Sparse representations of single cell dynamics

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1 Introduction

We want to obtain optimal reduced dimension representations of biological single cell tracking data. Such representations can for example be used to compare trajectories of different organisms and identify and quantify their common abstract features.

Motile microorganisms commonly have a preferred direction of motion on intermediate timescales while having highly stochastic behaviour on short timescales. This short timescale stochasiticity is the expected result of, for example the quasi random molecular dyanmics of actin filaments and myosin motors or the stochasitc growth, surface attachent and retraction of bacteria type IV pili (TFP).

We use ideas from the automated machine learning of the governing equations of physical systems from trajectory data, which works by obtaining sparse representations of a library of basis functions. This framework is extremely powerful and general but relies on the construction of a suitable library of basis functions in which the dynamics under examination are sparesly represented.

We start with the following auto regressive model of a biological unit with orientation $\boldsymbol{b} = b(\cos\theta, \sin\theta)$ and velocity $\boldsymbol{v}$,

$$\begin{aligned} v_{i+1}^{\parallel} &= q^{\parallel} v_i^{\parallel} + \ldots + a^{\parallel} \hat{\boldsymbol{n}}_{i+1} \\ v_{i+1}^{\perp} &= q^{\perp} v_i^{\perp} + \ldots + a^{\perp} \hat{\boldsymbol{n}}_{i+1} \\ \theta_{i+1} &= \theta_i + a_r \hat{\boldsymbol{n}}_{i+1} \end{aligned} \tag{1}$$

where $v_i^{\parallel} = (\boldsymbol{v}_i \cdot \boldsymbol{b}_i)$, $v_i^{\perp} = \boldsymbol{v}_i - v_i^{\parallel} \hat{\boldsymbol{b}}_i$.

2 Construct test data

3 Multiscale Entropy Analysis